

# Molecular Properties of Adult Mouse Gastric and Intestinal Epithelial Progenitors in Their Niches

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We sequenced 36,641 ESTs from laser capture microdissected adult mouse gastric and small intestinal epithelial progenitors and identified 4,031 and 3,324 unique transcripts that they express, respectively. Using Gene Ontology (GO) terms, each dataset was compared to cDNA libraries from intact adult stomach and small intestine. Genes in progenitor-enriched GO categories were filtered against genes in GO categories represented in hematopoietic, neural, and embryonic stem cell transcriptomes and mapped onto canonical signaling and metabolic pathways. The results reveal shared as well as distinctive features of adult gut stem cells.